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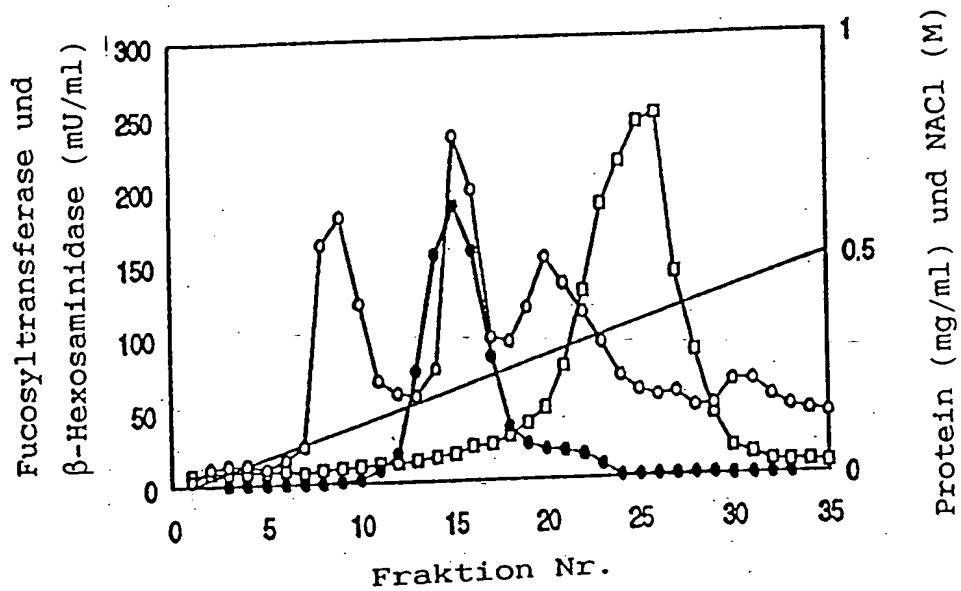


FIG. 1 a

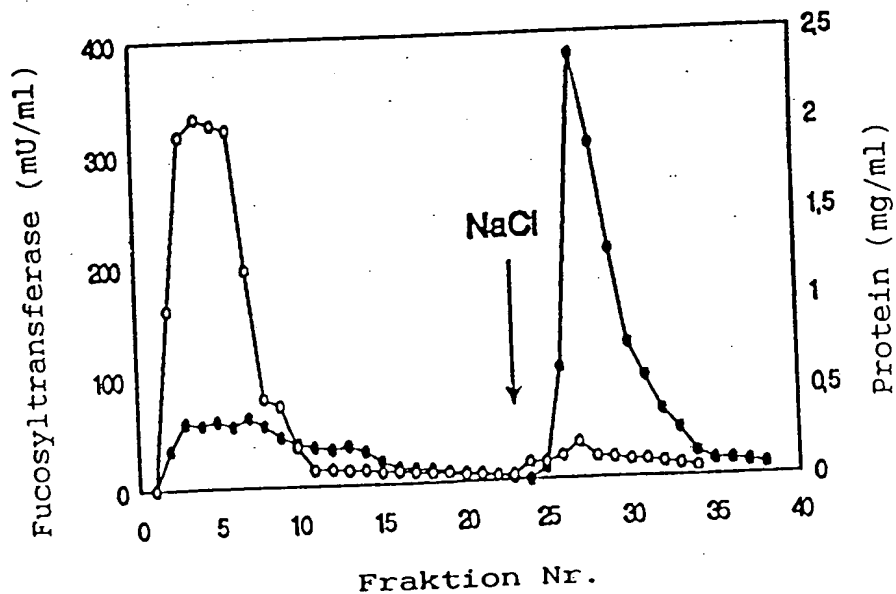


FIG. 1 b

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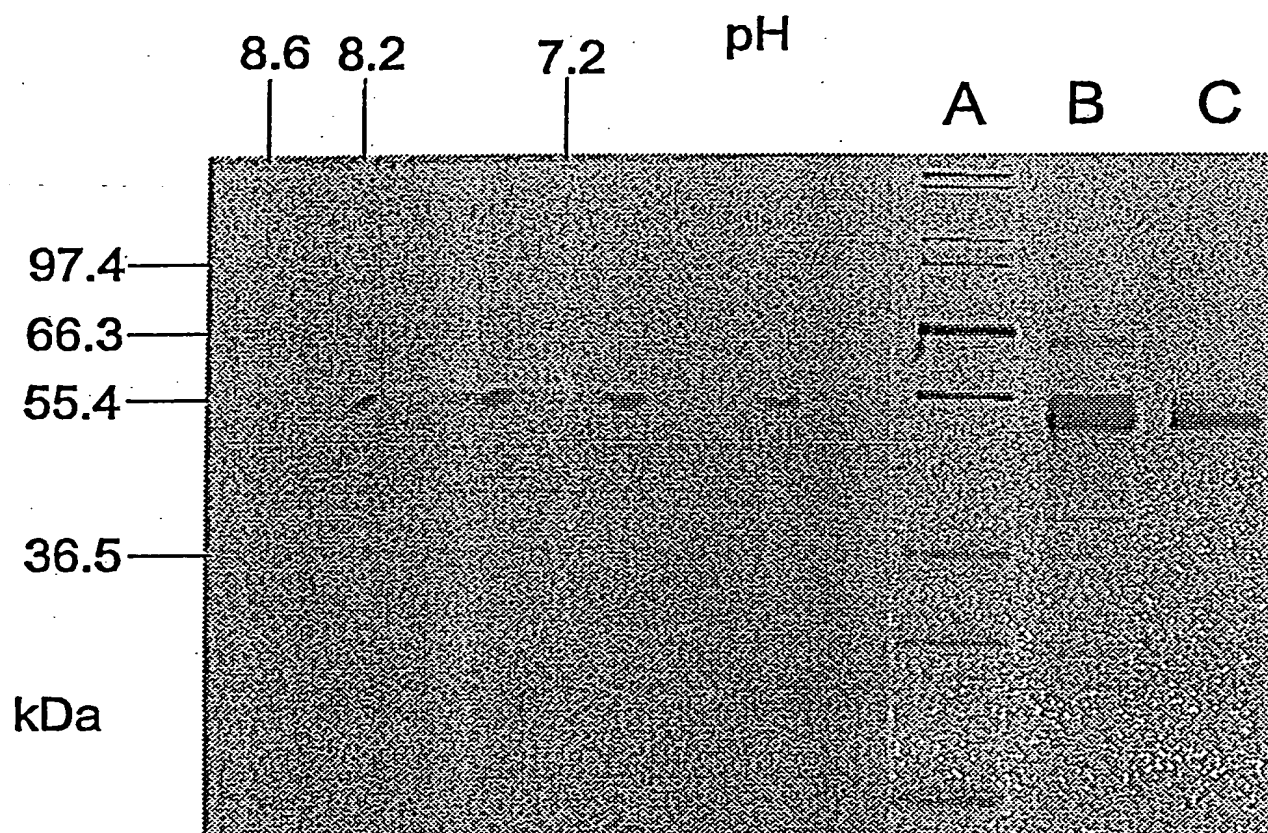
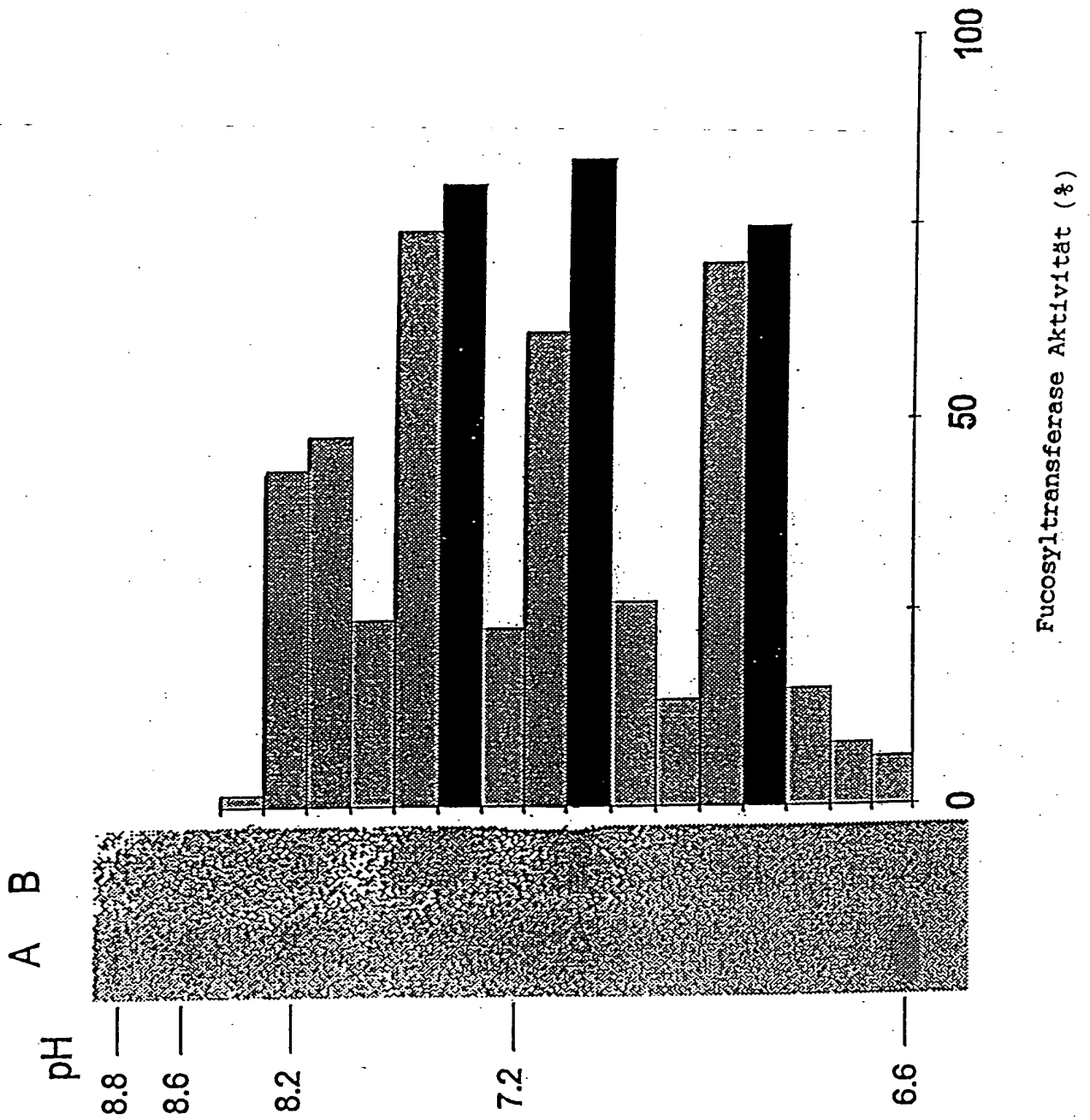


FIG.2

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FIG.3



- 1 KPDA_xFGLPQPSTAS
- 2 PETVYHIYVR
- 3 MESA EYYAENNIA
- 4 GRFEMESIYL

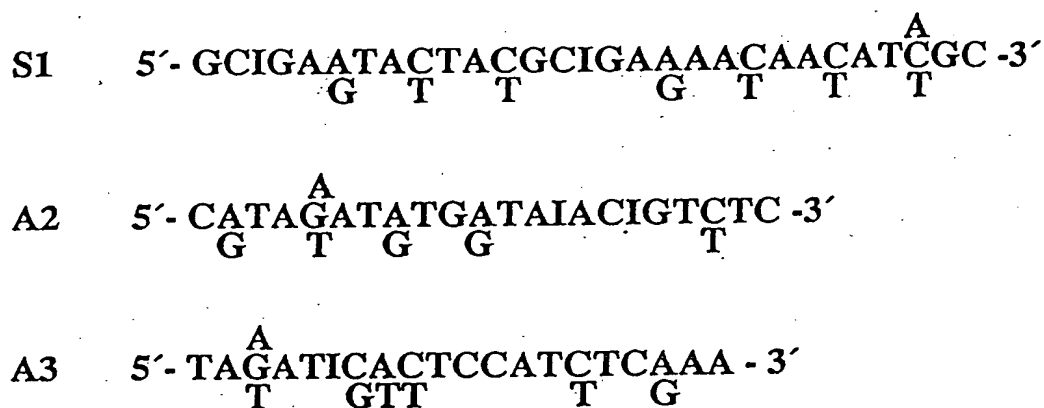


FIG.4

ACTAACTCAA ACGCTGCATT TTCTTTTTTC TTTCAGGGAA CCATCCACCC ATAACAACAA 60
 AAAAAACAAC AGCAAGCTGT GTTTTTTTTA TCGTTCCTTT TCTTTAAACA AGCACCCCCA 120
 TCATGGAATC GTGCTCATAA CGCCAAAATT TTCCATTTCC CTTTGATTTT TAGTTTATTT 180
 TGC GGAATTG GCAGTTGGGG GCGCAATTGA ATGATGGGTC TGGTGACGAA TCTTCGAGGC 240
 TCGAGAACAG ATGGTGCCCA ACAAGACAGC TTACCCGTTT TGGCTCCGGG AGGCAACCCA 300
 AAGAGGAAAT GGAGCAATCT AATGCCTCTT GTTGTTGCC TGTGTCAT CGCGGAGATC 360
 GCGTTTCTGG GTAGTTGGA TATGGCCAAA AACGCCGCCA TGGTTGACTC CCTCGCTGAC 420
 TTCTTCTACC GCTCTCGAGC GGTCGTTGAA GGTGACGATT TGGGGTTGGG TTTGGTGGCT 480
 TCTGATCGGA ATTCTGAATC GTATAGTTGT GAGGAATGGT TGGAGAGGGA GGATGCTGTC 540
 ACGTATTCGA GGGGCTTTTC CAAAGAGCCT ATTTTGTGTT CTGGAGCTGA TCAGGAGTGG 600
 AAGTCGTGTT CGGTTGGATG TAAATTTGGG TTTAGTGGGG ATAGAAAGCC AGATGCCGCA 660
 TTTGGGTTAC CTCAACCAAG TGGAACAGCT AGCATTCTGC GATCAATGGA ATCAGCAGAA 720
 TACTATGCTG AGAACAATAT TGCCATGGCA AGACGGAGGG GATATAACAT CGTAATGACA 780
 ACCAGTCTAT CTTCGGATGT TCCTGTTGGA TATTTTTCAT GGGCTGAGTA TGATATGATG 840
 GCACCAGTGC AGCCGAAAAC TGAAGCTGCT CTTGCAGCTG CTTTCATTTT CAATTGTGGT 900
 GCTCGAAATT TCCGGTTGCA AGCTCTTGAG GCCCTTGAAA AATCAAACAT CAAAATTGAT 960
 TCTTATGGTG GTTGTCACAG GAACCGTGAT GGAAGAGTGA ACAAAGTGGA AGCCCTGAAG 1020
 CACTACAAAT TTAGCTTAGC GTTTGAAAAT TCGAATGAGG AAGATTATGT AACTGAAAAA 1080
 TTCTTCCAAT CCCTTGTTGC TGGAAGTGTC CCTGTGGTTG TTGGTGCTCC AAATATTCAG 1140

FIG.5 a

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GACTTTGCTC	CTTCTCCTGG	TTCAATTTTA	CATATTAAAG	AGATAGAGGA	TGTTGAGTCT	1200
GTTGCAAAGA	CCATGAGATA	TCTAGCAGAA	AATCCCGAAG	CATATAATCA	ATCATTGAGG	1260
TGGAAGTATG	AGGGTCCATC	TGACTCCTTC	AAGGCCCTTG	TGGATATGGC	AGCTGTGCAT	1320
TCATCGTGCC	GTCTTTGCAT	TCACTTGGCC	ACAGTGAGTA	GAGAGAAGGA	AGAAAATAAT	1380
CCAAGCCTTA	AGAGACGTCC	TTGCAAGTGC	ACTAGAGGGC	CAGAAACCGT	ATATCATATC	1440
TATGTCAGAG	AAAGGGGAAG	GTTTGAGATG	GAGTCCATTT	ACCTGAGGTC	TAGCAATTTA	1500
ACTCTGAATG	CTGTGAAGGC	TGCTGTTGTT	TTGAAGTTCA	CATCCCTGAA	TCTTGTGCCT	1560
GTATGGAAGA	CTGAAAGGCC	TGAAGTTATA	AGAGGGGGGA	GTGCTTTAAA	ACTCTACAAA	1620
ATATACCCAA	TTGGCTTGAC	ACAGAGACAA	GCTCTTTATA	CCTTCAGCTT	CAAAGGTGAT	1680
GCTGATTTCA	GGAGTCACTT	GGAGAACAAT	CCTTGTGCCA	AGTTTGAAGT	CATTTTTGTG	1740
TAGCATGCGC	TAAATGGTAC	CTCTGCTCTA	CCTGAATTAG	CTTCACTTAG	CTGAGCACTA	1800
GCTAGAGTTT	TAGGAATGAG	TATGGCAGTG	AATATGGCAT	GGCTTTATTT	ATGCCTAGTT	1860
TCTTGGCCAA	CTCATTGATG	TTTTGTATAA	GACATCACAC	TTTAATTTTA	AACTTGTTTC	1920
TGTAGAAGTG	CAAATCCATA	TTTAATGCTT	AGTTTTAGTG	CTCTTATCTG	ATCATCTAGA	1980
AGTCACAGTT	CTTGTATATT	GTGAGTGAAA	ACTGAAATCT	AATAGAAGGA	TCAGATGTTT	2040
CACTCAAGAC	ACATTATTAC	TTCATGTTGT	TTTGATGATC	TCGAGCTTTT	TTAGTGTCTG	2100
GAACTGTCCC	TGTGGTTTGA	GCACCTGTTA	TTGCTTCAGT	GTTACTGTCC	AGTGGTTATC	2160
GTTTTTGACC	TCTAAAAAAA	AAAAAAAAAA	AAAAAAAAAA			2198

FIG.5 b

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Met Met Gly Leu Leu Thr Asn Leu Arg Gly Ser Arg Thr Asp Gly Ala
 1 5 10 15
 Gln Gln Asp Ser Leu Pro Val Leu Ala Pro Gly Gly Asn Pro Lys Arg
 20 25 30
 Lys Trp Ser Asn Leu Met Pro Leu Val Val Ala Leu Val Val Ile Ala
 35 40 45
 Glu Ile Ala Phe Leu Gly Arg Leu Asp Met Ala Lys Asn Ala Ala Met
 50 55 60
 Val Asp Ser Leu Ala Asp Phe Phe Tyr Arg Ser Arg Ala Val Val Glu
 65 70 75 80
 Gly Asp Asp Leu Gly Leu Gly Leu Val Ala Ser Asp Arg Asn Ser Glu
 85 90 95
 Ser Tyr Ser Cys Glu Glu Trp Leu Glu Arg Glu Asp Ala Val Thr Tyr
 100 105 110
 Ser Arg Gly Phe Ser Lys Glu Pro Ile Phe Val Ser Gly Ala Asp Gln
 115 120 125
 Glu Trp Lys Ser Cys Ser Val Gly Cys Lys Phe Gly Phe Ser Gly Asp
 130 135 140
 Arg Lys Pro Asp Ala Ala Phe Gly Leu Pro Gln Pro Ser Gly Thr Ala
 145 150 155 160
 Ser Ile Leu Arg Ser Met Glu Ser Ala Glu Tyr Tyr Ala Glu Asn Asn
 165 170 175
 Ile Ala Met Ala Arg Arg Arg Gly Tyr Asn Ile Val Met Thr Thr Ser
 180 185 190
 Leu Ser Ser Asp Val Pro Val Gly Tyr Phe Ser Trp Ala Glu Tyr Asp
 195 200 205
 Met Met Ala Pro Val Gln Pro Lys Thr Glu Ala Ala Leu Ala Ala Ala
 210 215 220
 Phe Ile Ser Asn Cys Gly Ala Arg Asn Phe Arg Leu Gln Ala Leu Glu
 225 230 235 240
 Ala Leu Glu Lys Ser Asn Ile Lys Ile Asp Ser Tyr Gly Gly Cys His

FIG.6 a

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Arg Asn Arg Asp Gly Arg Val Asn Lys Val Glu Ala Leu Lys His Tyr
 260 265 270
 Lys Phe Ser Leu Ala Phe Glu Asn Ser Asn Glu Glu Asp Tyr Val Thr
 275 280 285
 Glu Lys Phe Phe Gln Ser Leu Val Ala Gly Thr Val Pro Val Val Val
 290 295 300
 Gly Ala Pro Asn Ile Gln Asp Phe Ala Pro Ser Pro Gly Ser Ile Leu
 305 310 315 320
 His Ile Lys Glu Ile Glu Asp Val Glu Ser Val Ala Lys Thr Met Arg
 325 330 335
 Tyr Leu Ala Glu Asn Pro Glu Ala Tyr Asn Gln Ser Leu Arg Trp Lys
 340 345 350
 Tyr Glu Gly Pro Ser Asp Ser Phe Lys Ala Leu Val Asp Met Ala Ala
 355 360 365
 Val His Ser Ser Cys Arg Leu Cys Ile His Leu Ala Thr Val Ser Arg
 370 375 380
 Glu Lys Glu Glu Asn Asn Pro Ser Leu Lys Arg Arg Pro Cys Lys Cys
 385 390 395 400
 Thr Arg Gly Pro Glu Thr Val Tyr His Ile Tyr Val Arg Glu Arg Gly
 405 410 415
 Arg Phe Glu Met Glu Ser Ile Tyr Leu Arg Ser Ser Asn Leu Thr Leu
 420 425 430
 Asn Ala Val Lys Ala Ala Val Val Leu Lys Phe Thr Ser Leu Asn Leu
 435 440 445
 Val Pro Val Trp Lys Thr Glu Arg Pro Glu Val Ile Arg Gly Gly Ser
 450 455 460
 Ala Leu Lys Leu Tyr Lys Ile Tyr Pro Ile Gly Leu Thr Gln Arg Gln
 465 470 475 480
 Ala Leu Tyr Thr Phe Ser Phe Lys Gly Asp Ala Asp Phe Arg Ser His
 485 490 495
 Leu Glu Asn Asn Pro Cys Ala Lys Phe Glu Val Ile Phe Val
 500 505 510

FIG.6 b

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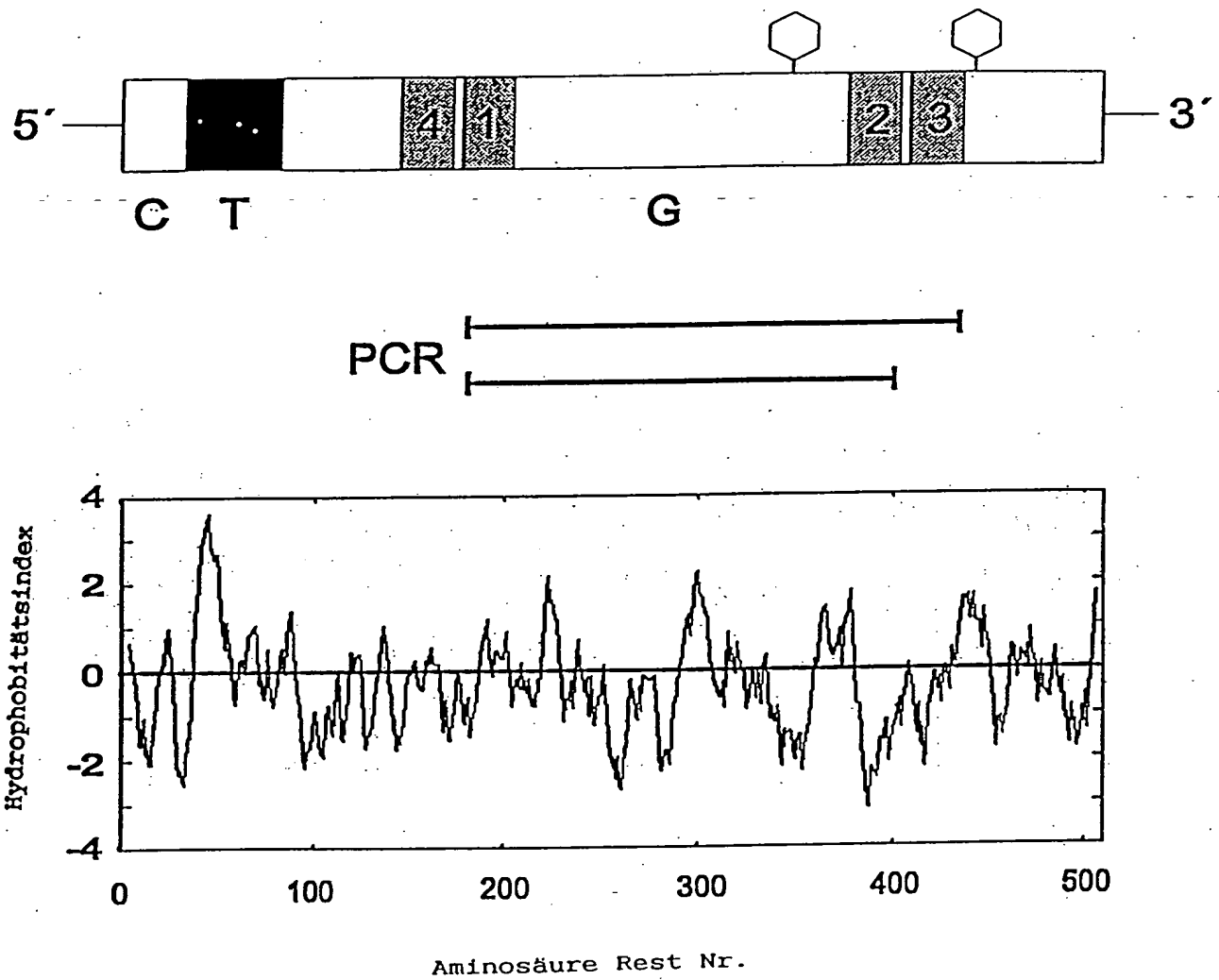


FIG.7

Transferase	Art	# ^a	konserviertes Motiv
FucT-C3	Mungo Bohne	267	-EALKHYKFSIAFENSNEEDYVTEKFFQ-SLVAGTVP
FucT-III	Mensch	P21217	236-ETLSRYKFYLAFENSLHPDYITEKLWRNALEAWAVP
FucT-III	Schimpanse	O19058	247-ETLSRYKFYLAFENSLHPDYITEKLWRNALEAWAVP
FucT-V	Mensch	Q11128	249-ETLSRYKFYLAFENSLHPDYITEKLWRNALEAWAVP
FucT-V	Schimpanse	P56433	249-ETLSRYKFYLAFENSLHPDYITEKLWRNALEAWAVP
FucT-VI	Mensch	P51993	235-ETLSRYKFYLAFENSLHPDYITEKLWRNALEAWAVP
FucT-VI	Schimpanse	P56434	235-ETLSRYKFYLAFENSLHPDYITEKLWRNALEAWAVP
FucT-III	Rind	Q11126	240-KQLSQKFYLAFENSLHPDYITEKLWRNALQAWAVP
FucT-?	chin. Hamster	O35886	237-GTLARYKFYLAFENSLHPDYITEKLWKNALEAWAVP
FucT-VII	Mensch	Q11130	217-PTVAQYRFYLSFENSQHRDYITEKFWRNALVAGTVP
FucT-VII	Maus	Q11131	264-PTLARYRFYLAFENSQHRDYITEKFWRNALVAGTVP
FucT-VII	Schistosoma mansoni	O76204	226-PTLARYRFYLAFENSQHRDYITEKFWRNALVAGTVP
FucT-IV	Mensch	P22083	277-HTVARYKFYLAFENSQHLDYITEKLWRNALLAGAVP
FucT-IV	Maus	Q11127	305-HTVARYKFYLAFENSQRHVDYITEKLWRNAFLAGAVP
FucT-IV	Ratte	Q62994	305-HTVARYKFYLAFENSQHVDYITEKLWRNAFLAGAVP
FucT-IV	Huhn	Q98952	228-KTVSAYKFYLAFENSQHTDYITEKLWKNAFAASAVP
FucT-IX	Maus	O88819	233-PTISTCKFYLSFENSQHKDYITEKLYNAFL-AGSVP
FutA	Dictyostelium discoideum	O76544	247-DVLKRYNEALAFENSLCKDYITEKLWE-SLSVGTIP
hpFucT1	Helicobacter pylori	O32631	106-EFLSQKFNLCFENSQGYGYVTEKILD-AYFSHTIP
hpFucT2	Helicobacter pylori	O30511	227-EFLSQKFNLCFENTQGYGYVTEKIID-AYFSHTIP
CEFT-1	Caenorhabditis elegans	Q21362	303-MLDTDYHFYVTFENSICEDYVTEKLWKSQYQNTIIP

^a Zugriffsnummer für die SwissProt Protein Sequenz Datenbank

FIG.8

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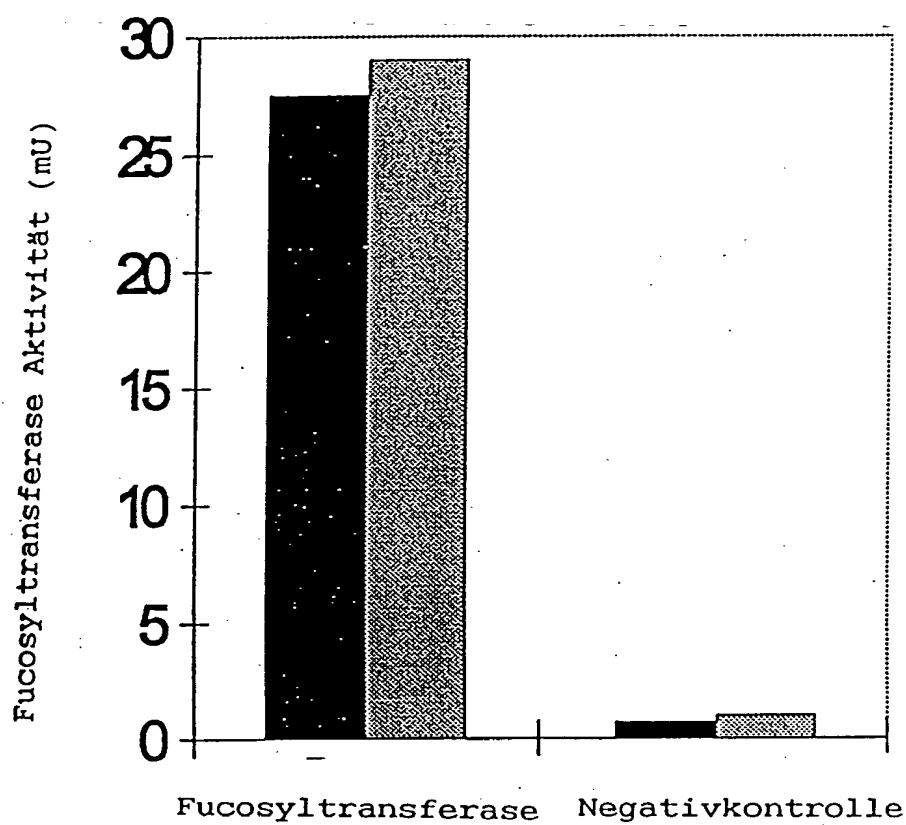


FIG.9

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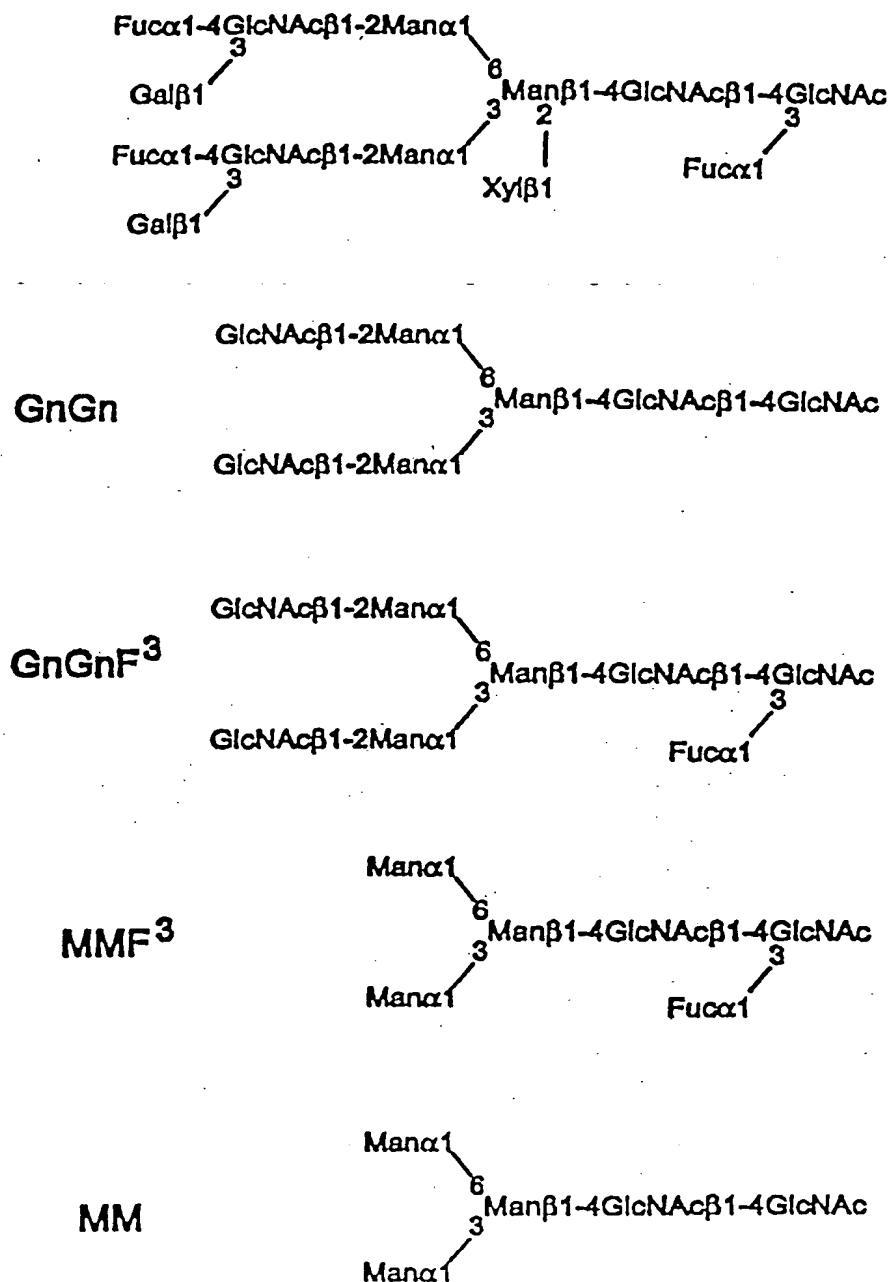


FIG.10 a

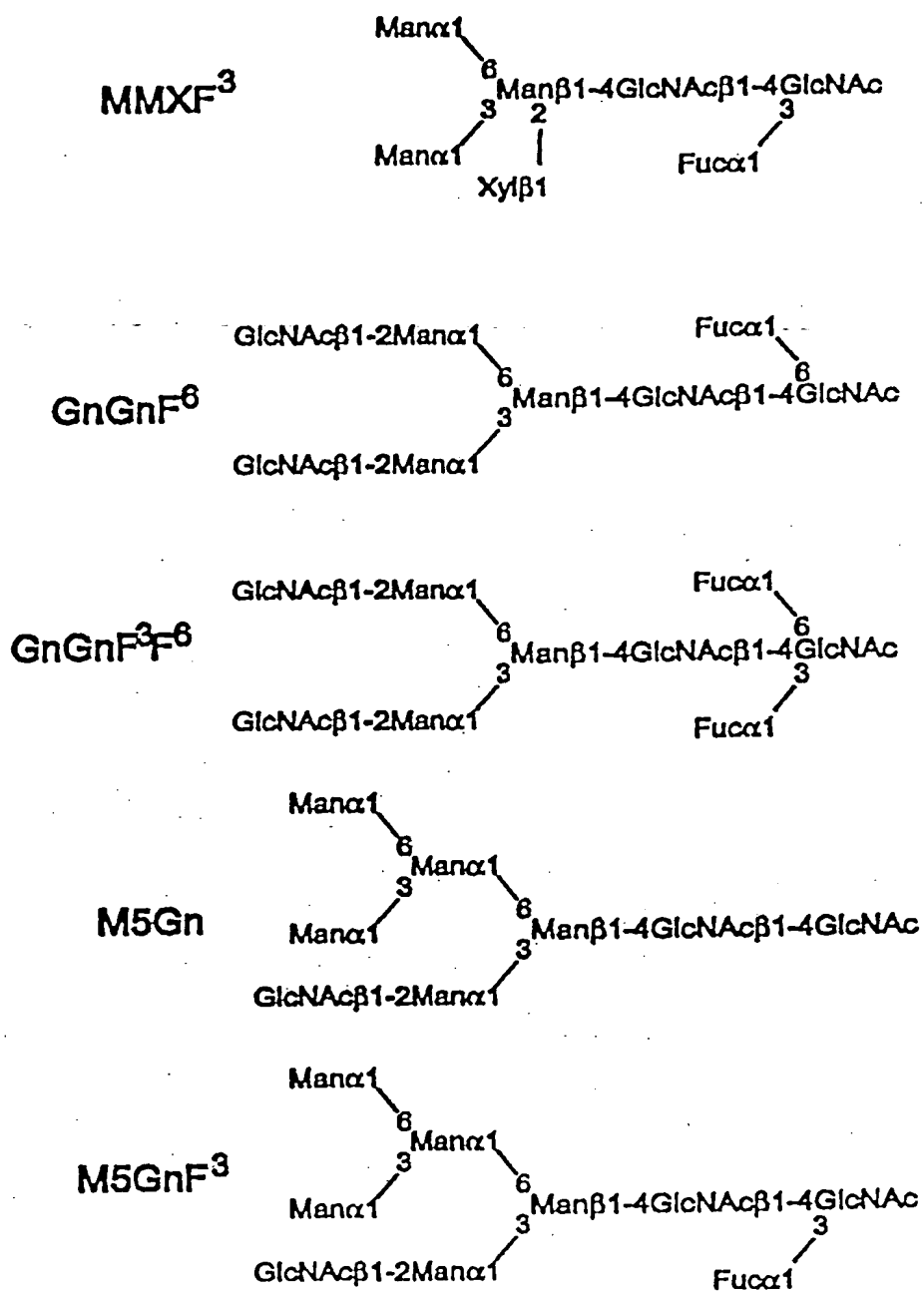


FIG.10 b

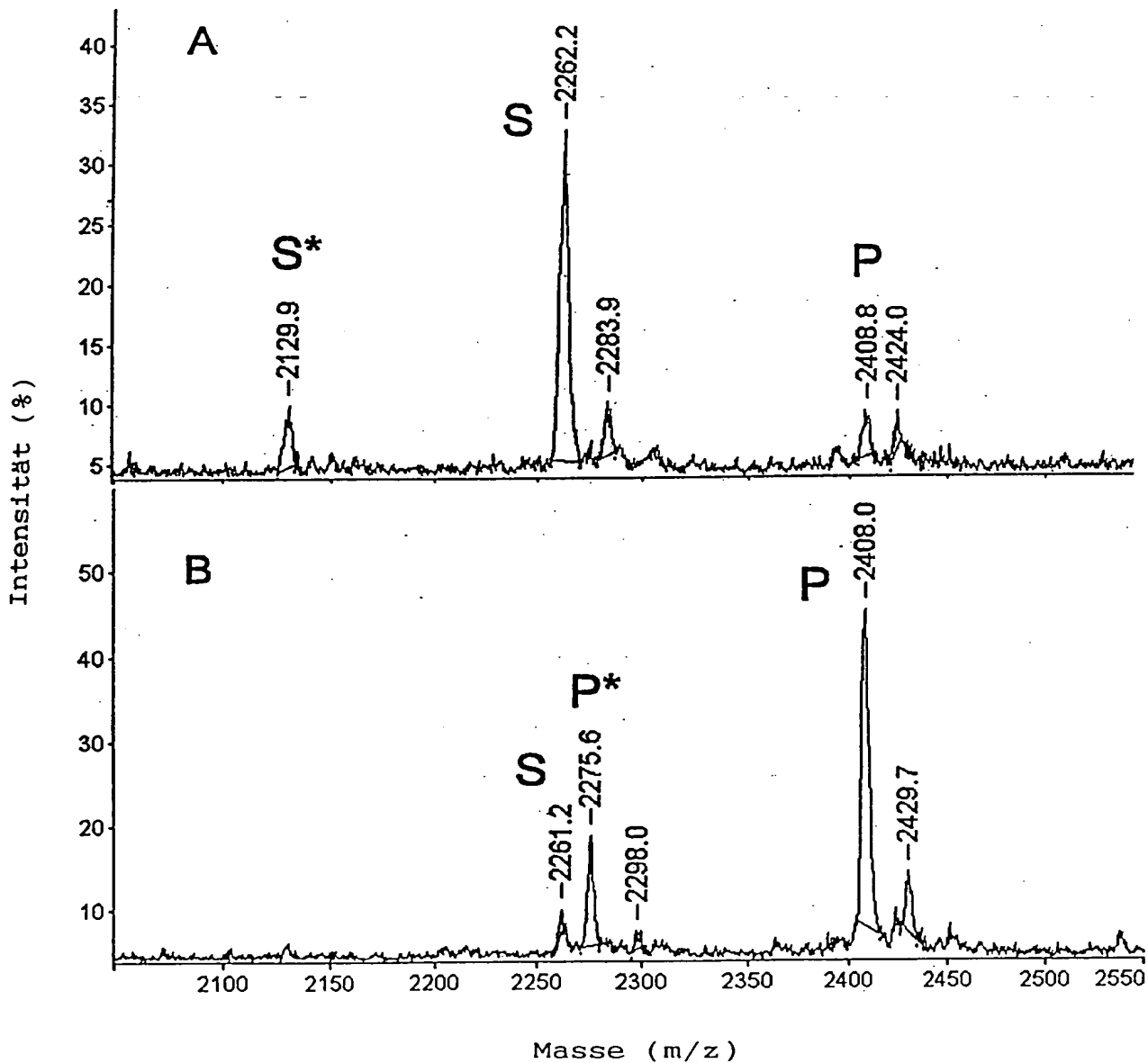
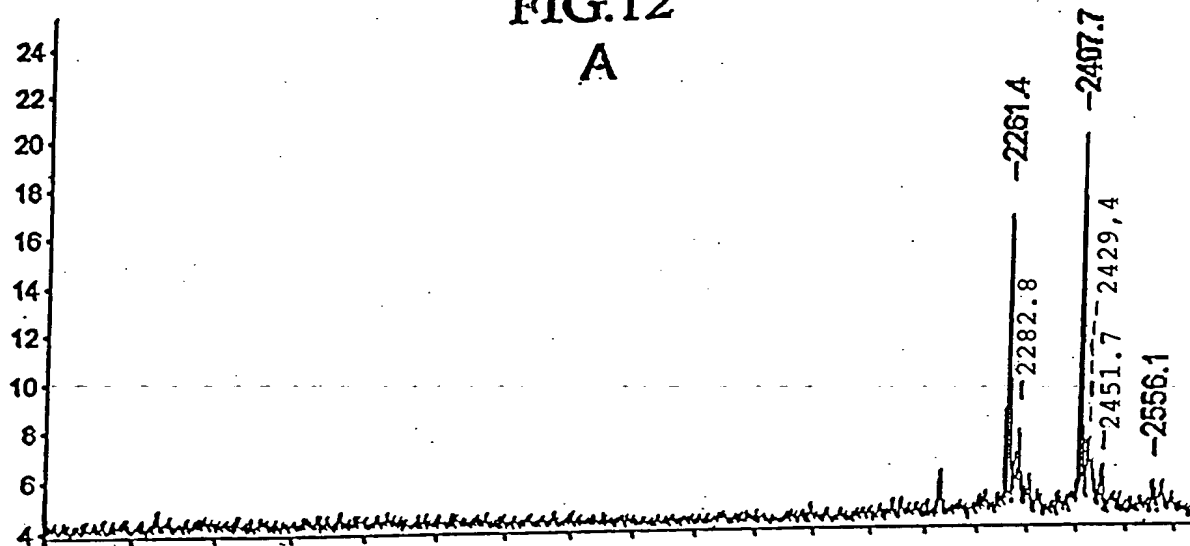


FIG.11

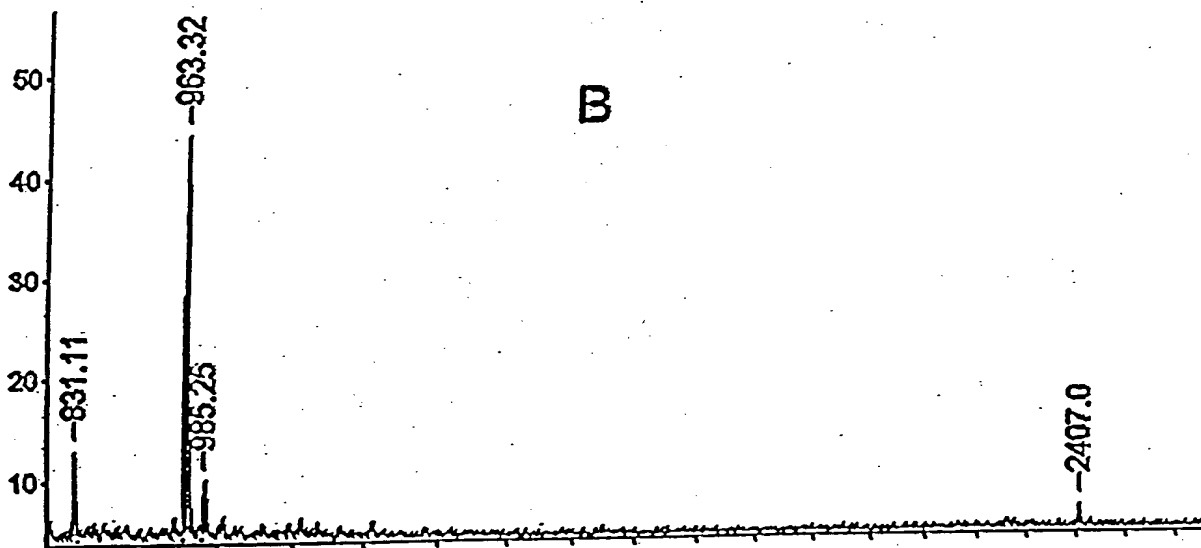
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FIG.12

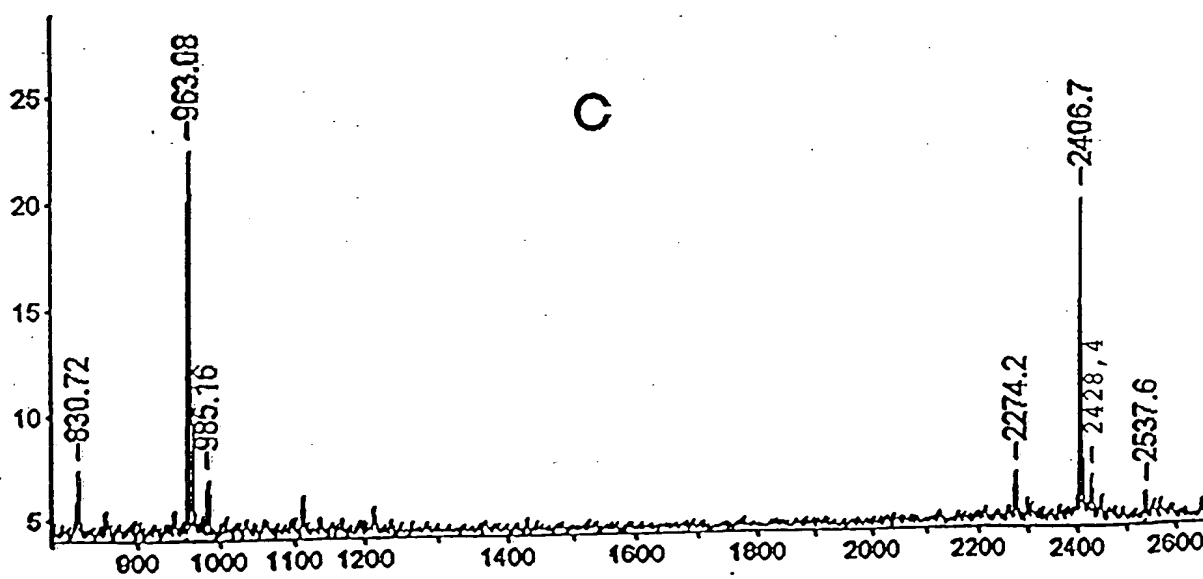
A



B



C



Masse (m/z)

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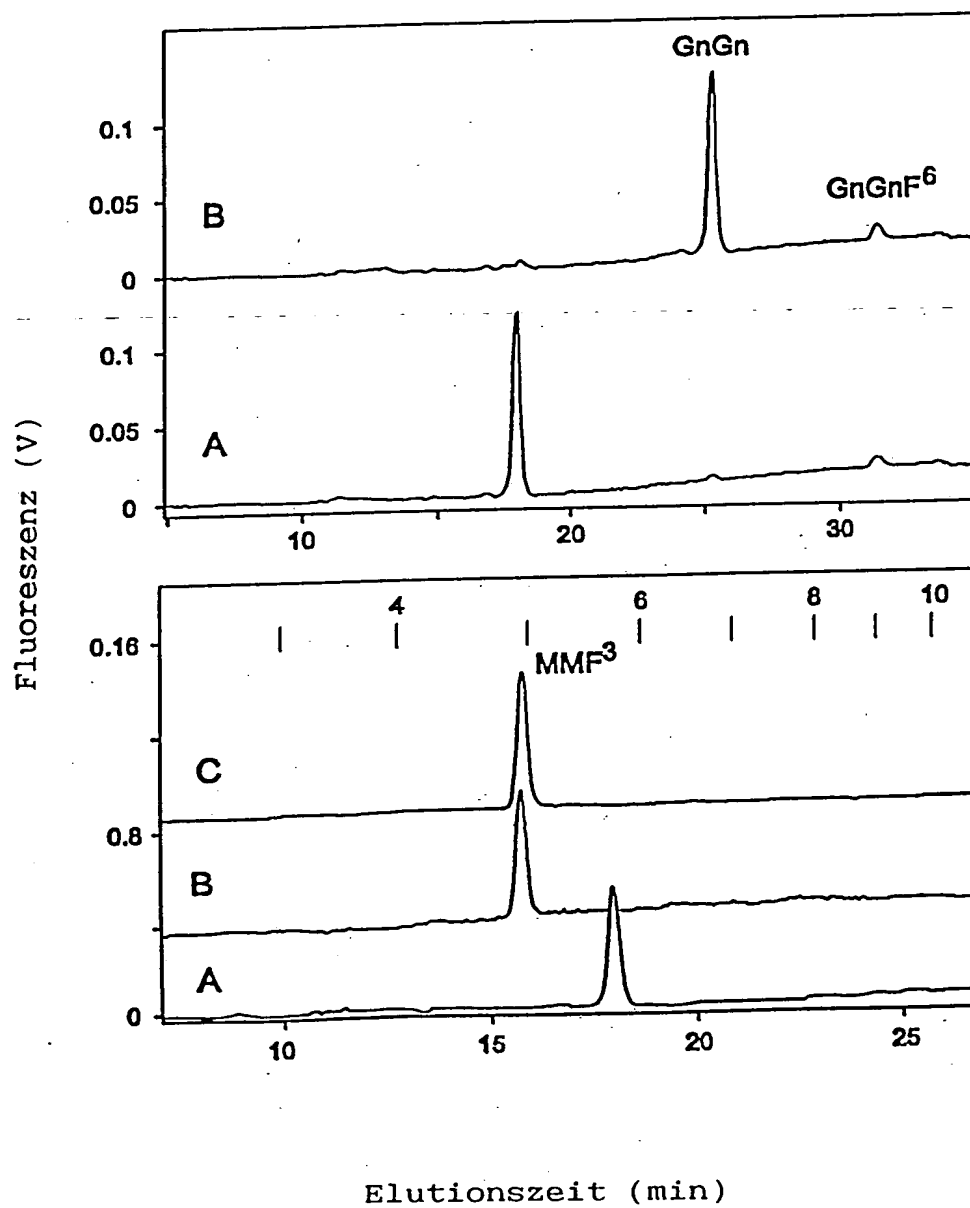


FIG. 13